

REPLACEMENT SHEET

Figure 1

MAMSSGGSGGGVPEQEDSVLFRRGTGQSDDSDIWDDTALIKAYDKAVASFKHALKNG
DICETSGKPKTTPKRKPAKKNKSQKKNTAASLQQWKVGDKCSAIWSEDGCIYPATIA
SIDFKRETCVVVYTGYGNREEQNLSDLLSPICEVANNIEQNAQENENESQVSTDESE
NSRSPGNKSDNIKPKSAPWNSFLPPPPMPGPRLGPGKPGGLKFNGPPPPPPPPPHL
LSCWLPPFPSPGPIIPPPPPICPDSLDDADALGSMLISWYMSGYHTGYMGRQNQK
EGRCSHSLN



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REPLACEMENT SHEET

Figure 2B



AATTTTAAATTTTTGTAGAGACAGGGTCTCATTATGTTGCCCAGGGTGGTGTCAA
GCTCCAGGTCTCAAGTGATCCCCCTACCTCCGCCTCCCAAAGTTGTGGGATTGTAGG
CATGAGCCACTGCAAGAAAACCTTAACTGCAGCCTAATAATTGTTTTCTTTGGGATA
ACTTTTAAAGTACATTAAAAGACTATCAACTTAATTTCTGATCATATTTTGTGGAAT
AAAATAAGTAAAATGTCTTGTGAACAAAATGCTTTTTAACATCCATATAAAGCTATC
TATATATAGCTATCTATATCTATATAGCTATTTTTTTTAACTTCCTTTTATTTTCCT
TACAG*GGTTTTAGACAAAATCAAAAAGAAGGAAGGTGCTCACATTCCTTAAATTAA
GGA*GTAAGTCTGCCAGCATTATGAAAGTGAATCTTACTTTTGTAAAACCTTTATGGT
TTGTGGAAAACAAATGTTTTTGAACAGTTAAAAAGTTCAGATGTTAGAAAGTTGAAA
GGTTAATGTAAAACAATCAATATTAAAGAATTTTGATGCCAAAACCTATTAGATAAAA
GGTTAATCTACATCCCTACTAGAATTCTCATACTTAACTGGTTGGTTGTGTGGAAGA
AACATACTTTCACAATAAAGAGCTTTAGGATATGATGCCATTTTATATCACTAGTAG
GCAGACCAGCAGACTTTTTTTTATTGTGATATGGGATAACCTAGGCATACTGCACTG
TACACTCTGACATATGAAGTGCTCTAGTCAAGTTTAACTGGTGTCCACAGAGGACAT
GGTTTAACTGGAATTCGTCAAGCCTCTGGTTCTAATTTCTCATTTGCAG*GAAATGC
TGGCATAGAGCAGCACTAAATGACACCACTAAAGAAACGATCAGACAGATCTGGAAT
GTGAAGCGTTATAGAAGATAACTGGCCTCATTTCTTCAAAATATCAAGTGTTGGGAA
AGAAAAAAGGAAGTGGAATGGGTAACTCTTCTTGATTAAAAGTTATGTAATAACCAA
ATGCAATGTGAAATATTTTACTGGACTCTTTTGAAAAACCATCTGTAAAAGACTGAG
GTGGGGGTGGGAGGCCAGCACGGTGGTGAGGCAGTTGAGAAAATTTGAATGTGGATT
AGATTTTGAATGATATTGGATAATTATTGGTAATTTTATGGCCTGTGAGAAGGGTGT
TGTAGTTTATAAAAGACTGTCTTAATTTGCATACTTAAGCATTTAGGAATGAAGTGT
TAGAGTGTCTTAAAATGTTTCAAATGGTTTAAACAAAATGTATGTGAGGCGTATGTGG
CAAAATGTTACAGAATCTAACTGGTGGACATGGCTGTTTCATTGTACTGTTTTTTCT
ATCTTCTATATGTTTTAAAAGTATATAATAAAAATATTTAATTT

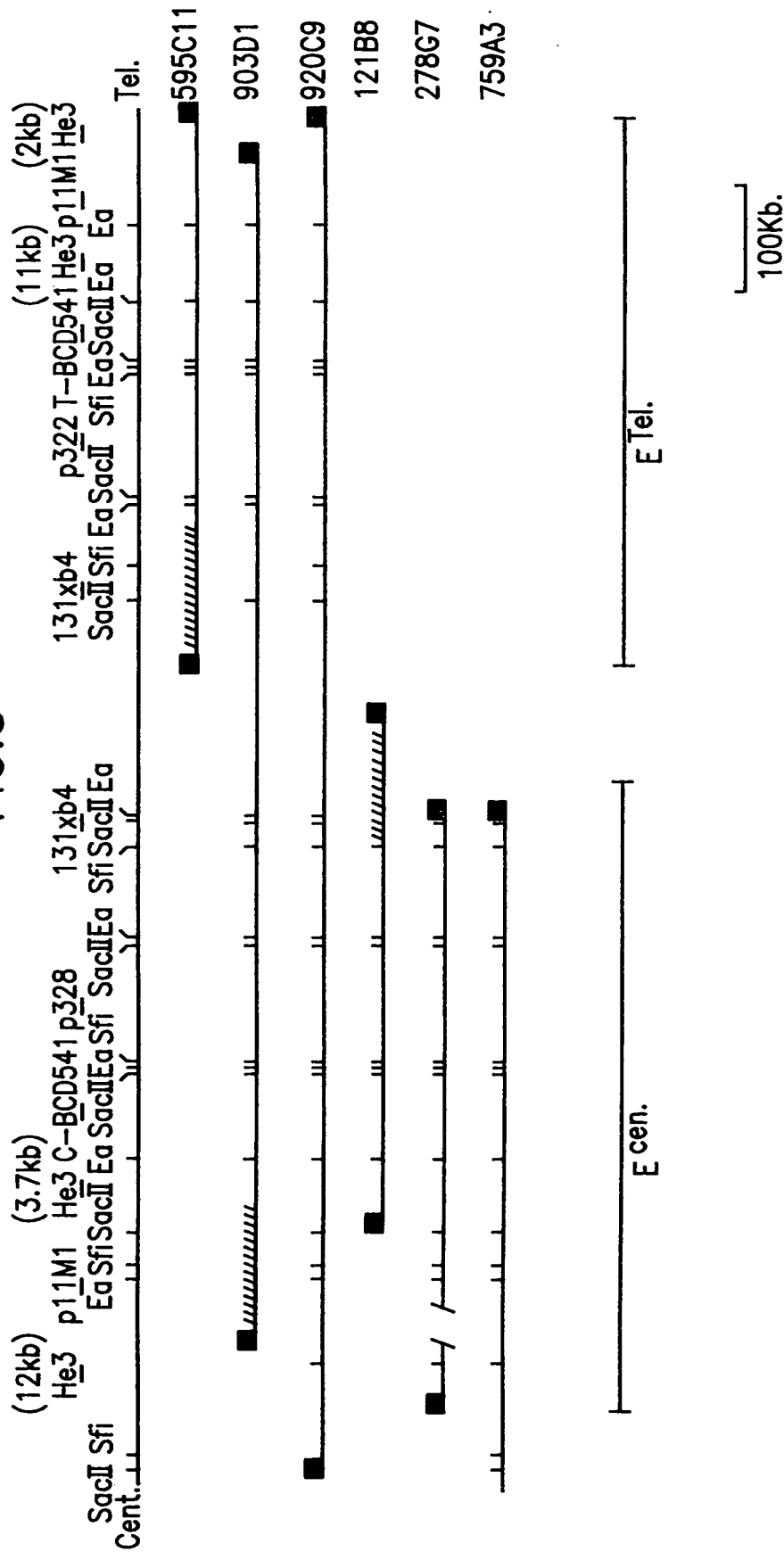


Figure 3B

AATTTTAAATTTTTGTAGAGACAGGGTCTCATTATGTTGCCCAGGGTGGTGTCAA
GCTCCAGGTCTCAAGTGATCCCCCTACCTCCGCCTCCCAAAGTTGTGGGATTGTAGG
CATGAGCCACTGCAAGAAAACCTTAACTGCAGCCTAATAATTGTTTTCTTTGGGATA
ACTTTTAAAGTACATTAAAAGACTATCAACTTAATTTCTGATCATATTTTGTGAAT
AAAATAAGTAAAATGTCTTGTGAACAAAATGCTTTTTTAACATCCATATAAAGCTATC
TATATATAGCTATCTATGTCTATATAGCTATTTTTTTTAACTTCCTTTTATTTTCCT
TACAG*GGTTTCAGACAAAATCAAAAAGAAGGAAGGTGCTCACATTCCTTAAATTAA
GGA*GTAAGTCTGCCAGCATTATGAAAGTGAATCTTACTTTTGTAAACTTTATGGT
TTGTGGAAAACAAATGTTTTTGAACAGTTAAAAAGTTCAGATGTTAAAAAGTTGAAA
GGTTAATGTAAAACAATCAATATTAAAGAATTTTGATGCCAAAACCTATTAGATAAAA
GGTTAATCTACATCCCTACTAGAATTCTCATACTTAACTGGTTGGTTATGTGGAAGA
AACATACTTTCACAATAAAGAGCTTTAGGATATGATGCCATTTTATATCACTAGTAG
GCAGACCAGCAGACTTTTTTTTTATTGTGATATGGGATAACCTAGGCATACTGCACTG
TACACTCTGACATATGAAGTGCTCTAGTCAAGTTTAACTGGTGTCCACAGAGGACAT
GGTTTAACTGGAATTCGTCAAGCCTCTGGTTCTAATTTCTCATTTGCAG*GAAATGC
TGGCATAGAGCAGCACTAAATGACACCCTAAAGAAACGATCAGACAGATCTGGAAT
GTGAAGCGTTATAGAAGATAACTGGCCTCATTTCTTCAAAATATCAAGTGTGGGAA
AGAAAAAAGGAAGTGGAATGGGTAACCTCTTCTTGATTAAAAGTTATGTAATAACCAA
ATGCAATGTGAAATATTTTACTGGACTCTTTTGAAAAACCATCTGTAAAAGACTGGG
GTGGGGGTGGGAGGCCAGCACGGTGGTGAGGCAGTTGAGAAAATTTGAATGTGGATT
AGATTTTGAATGATATTGGATAATTATTGGTAATTTTATGGCCTGTGAGAAGGGTGT
TGTAGTTTATAAAAGACTGTCTTAATTTGCATACTTAAGCATTTAGGAATGAAGTGT
TAGAGTGTCTTAAAATGTTTCAAATGGTTTAAACAAAATGTATGTGAGGCGTATGTGG
CAAAATGTTACAGAATCTAACTGGTGGACATGGCTGTTTATTGTACTGTTTTTTTCT
ATCTTCTATATGTTTAAAAGTATATAATAAAAATATTTAATTT

TCCACCCGCCTTGGCCTCCCAAAGCNCTGGGATTACAGGCGTGACTGCCGCACCCAG
CTGTAAACTGGNTTNNTAATGGTAGATTTTNAGGTATTAACAATAGATAAAAAGATA
CTTTTNGGCATACTGTGTATTGGGATGGGGTTAGAACAGGTGTNCTACCCAAGACAT
TACTTAAAATCGCCCTCGAAATGCTATGTGAGCTGTGTGTGTGTGTGTGTGTGTGT
GTGTATTAAAGGAAAAGCATGAAAGTATTTATGCTTGATTTTTTTTTTTTNACTCATAG
CTTCATAGTGGANCAGATACATAGTCTAAATCAAAATGTTTAAACTTTTTATGTCAC
TTGCTGTC

Fig. 5



Restriction map of the 5q13 region for EagI(Ea), SacII(SacII), SfiI(Sfi). Numbers under parenthesis indicate the restriction fragment detected by He3; Telomeric element (E Tel), centromeric element (Ecen), Centromer(Cent.), Telomere(Tel.). Probes are indicated above the restriction map. YACS are below the restriction map.



FIG.6



Telomeric element (E^{Tel}) containing the survival motor-neuron gene (SMN gene). Genetic map shows polymorphic markers C212, C272 and C171. Physical map shows location and direction of transcription of SMN gene; phage clones used for assembling physical map. Restriction map for EcoRI(E), XbaI(X), HindIII(H), BglII(B), SacII(S) are shown. Cent. and Tel. indicate centromere and telomere respectively. The position of genomic rearrangements found in SMA patients are also indicated.



GENE DOSAGE ANALYSIS OF THE 5q13 REGION WITH THE 132SE11 PLASMID CONE IN SMA TYPE I PATIENT. TOTAL HUMAN DNA FROM SMA FAMILY WAS DIGESTED WITH HindIII FOR SOUTHERN BLOTTING. FILTER WAS CONSECUTIVELY HYBRIDIZED WITH 132SE11 (A) AND JK53 PROBES (B). A SIGNIFICANT DECREASE IN 132SE11 BAND INTENSITY, WHICH INDICATED THE DELETION, COMPARED WITH THEIR PARENTS. F/FATHER, M/MOTHER, A/AFFECTED

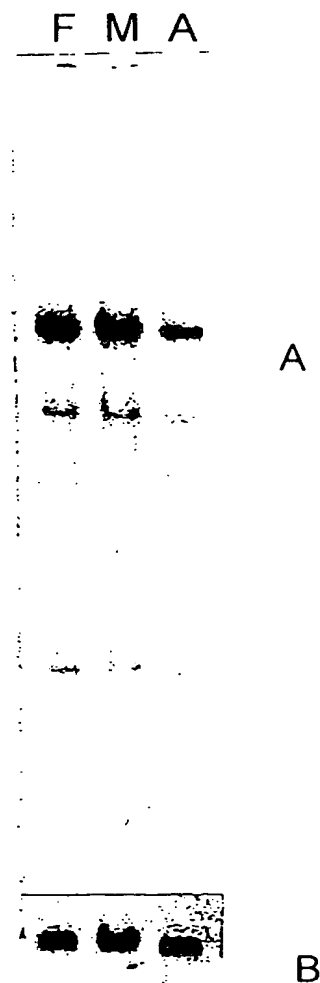


FIG. 7



REPLACEMENT SHEET

Figure 8

MAMSSGGSGGGVPEQEDSVLFRRGTGQSDDSDIWDDTALIKAYDKAVASFKHALKNG
DICETSGKPKTTPKRKPAKKNSQKKNTAASLQQWKVGDKCSAIWSEDGCIYPATIA
SIDFKRETCVVVYTGYGNREEQNLSDLLSPICEVANNIEQNAQENENESQVSTDESE
NSRSPGNKSDNIKPKSAPWNSFLPPPPMPGPRLGPGKPGGLKFNGPPPPPPPPPHL
LSCWLPPFPSPGPPIIPPPPPICPDSLDDADALGSMLISWYMSGYHTGYM

[illegible]



REPLACEMENT SHEET

Figure 10A

1

cctccccgggcaccgtactgttccgctcccagaagccccgggcccgaagtcgtcac
tcttaagaaggacggggccccacgctgcgcacccgcgggtttgct ATG GCG

M A

ATG AGC AGC GGC GGC AGT GGT GGC GGC GTC CCG GAG CAG GAG
M S S G G S G G G V P E Q E
GAT TCC GTG CTG TTC CGG CGC GGC ACA GGC CAG gtgaggtcgcagc
D S V L F R R G T G Q

cagtgcagtcctccctatttagcgctctcagcacccttcttccggcccaactctccttc
cgca

2a

gtgtaattttgttatgtgtggattaagatgactcttggtactaacatacattttctg
attaaacctatctgnacatgagttgtttttattttcttaccctttccag AGC GAT

S D

GAT TCT GAC ATT TGG GAT GAT ACA GCA CTG ATA AAA GCA TAT
D S D I W D D T A L I K A Y
GAT AAA GCT GTG GCT TCA TTT AAG gtatgaaatgcttgnttagtcgttt
D K A V A S F K

tcttattttctcgtttatttcatttggaaggaattgataacatacgataaagtgttaa

2b

aggtgctttctgagggtgacggagccttgagactagcttatagtagtaactgggttat
gtcgtgacttttatttctgtgcaccaccctgtaacatgtacatttttattcctatttt
cgtag CAT GCT CTA AAG AAT GGT GAC ATT TGT GAA ACT TCG GGT

H A L K N G D I C E T S G

AAA CCA AAA ACC ACA CCT AAA AGA AAA CCT GCT AAG AAG AAT
K P K T T P K R K P A K K N
AAA AGC CAA AAG AAG AAT ACT GCA GCT TCC TTA CAA CAG gttat
K S Q K K N T A A S L Q Q

tttaaaatgttgaggatttaacttcaaaggatgtctcattagtccttattttaatagt
gtaaaatgtctttaact

3

gcctgcagggtcgatcaaaacgagatgatagtttgccctcttcaaaagaaatgtgtgc
atgtatatatctttgatttctttttag TGG AAA GTT GGG GAC AAA TGT

W K V G D K C

TCT GCC ATT TGG TCA GAA GAC GGT TGC ATT TAC CCA GCT ACC
S A I W S E D G C I Y P A T
ATT GCT TCA ATT GAT TTT AAG AGA GAA ACC TGT GTT GTG GTT
I A S I D F K R E T C V V V
TAC ACT GGA TAT GGA AAT AGA GAG GAG CAA AAT CTG TCC GAT
Y T G Y G N R E E Q N L S D
CTA CTT TCC CCA ATC TGT GAA GTA GCT AAT AAT ATA GAA CAG
L L S P I C E V A N N I E Q



REPLACEMENT SHEET

Figure 10B

AAT GCT CAA GAG gtaaggatacaaaaaaaaaaaaaattcaatttctggaagcag
N A Q E
agactagatgagaaactgttaaacagtatacaca

4

ccaccgaggcattaatttttttcttaatcacacccttataacaaaaacctgcatattt
tttcttttttaaag AAT GAA AAT GAA AGC CAA GTT TCA ACA GAT GAA
N E N E S Q V S T D E
AGT GAG AAC TCC AGG TCT CCT GGA AAT AAA TCA GAT AAC ATC
S E N S R S P G N K S D N I
AAG CCC AAA TCT GCT CCA TGG AAC TCT TTT CTC CCT CCA CCA
K P K S A P W N S F L P P P
CCC CCC ATG CCA GGG CCA AGA CTG GGA CCA GGA AAG gtaaaccctt
P P M P G P R L G P G K
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aatttgtagctctccca

5

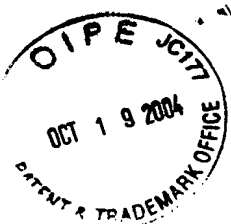
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catattgaaattggtaagttaattttccttttgaaatatccttatag CCA GGT
P G
CTA AAA TTC AAT GGC CCA CCA CCG CCA CCG CCA CCA CCA CCA
L K F N G P P P P P P P P P
CCC CAC TTA CTA TCA TGC TGG CTG CCT CCA TTT CCT TCT GGA
P H L L S C W L P P F P S G
CCA CCA gtaagtaaaaaagagtataggtagatttttgctttcacatacaatttga
P P
taatta

6

ccagacttttaattttttggtttactggatataaacaatatcttttttctgtctccag
ATA ATT CCC CCA CCA CCT CCC ATA TGT CCA GAT TCT CTT GAT
I I P P P P P I C P D S L D
GAT GCT GAT GCT TTG GGA AGT ATG TTA ATT TCA TGG TAC ATG
D A D A L G S M L I S W Y M
AGT GGC TAT CAT ACT GGC TAT TAT ATG gtaagtaatcactcagcatct
S G Y H T G Y Y M
tttcctgacaattttttttagttatgtgactttgtttggtaaatttataaaataact
acttg

7

aactgcagcctaataattgtttttctttgggataactttttaagtacattaaaagact
atcaacttaatttctgatcatattttgttgaataaaaataagtaaaatgtcttgtgaa



REPLACEMENT SHEET

Figure 10C

→ a
acaaaatgctttttaacatccatataaagctatctatatatagctatctatgtctat

→ T
atagctatttttttaacttccttttattttccttacag GGT TTC AGA CAA
G F R Q
AAT CAA AAA GAA GGA AGG TGC TCA CAT TCC TTA AAT taaggagta
N Q K E G R C S H S L N *
aagtctgccagcattatgaaagtgaatcttacttttgtaaaacttttatggtttggtg

→ g
aaaacaaatgtttttgaacagttaaaaagttcagatgttaa~~aaa~~agttgaaaggtttaa
tgtaaaacaatcaatatttaaagaattttgatgccaaaactattagataaaaggtttaa

→ g
tctacatccctactagaattctcatacttaactggttggttatgtggaagaaacata
ctttcacaataaagagagcttttaggatatgatgccattttatatcactagtaggcagac
cagcagacttttttttattgtgatatgggataacctaggcatactgcactgtacact
ctgacatatgaagtgtcttagtcaagtttaactgggtgtccacagaggacatggttta

8
actggaattcgtcaagcctctggtttctaattttctcatttgcaggaaatgctggcata
gagcagcactaaatgacaccactaaagaaacgatcagacagatctggaatgtgaagc
gttatagaagataactggcctcattttcttcaaaatatcaagtgttgggaaagaaaaa
aggaagtggaatgggtaactcttcttgattaaaagttatgtaataaccaaatagcaat

→ a
gtgaaatattttactggactcttttgaaaaaccatctagtaaaagactg~~gg~~gtgggg
gtgggaggccagcacggtggtgaggcagttgagaaaatttgaatgtggattagattt
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gtcttaaaatgtttcaaagtgtttaacaaaatgtatgtgaggcgtatgtggcaaat
gttacagaatctaactgggtggacatggctgttcattgtactgtttttttctatcttc
tatatgttttaaagtatata~~aata~~aaaatattta



REPLACEMENT SHEET

Figure 11

gatctgccttccttcctgcccccatgtttgtctttccttggtttgtcttta 50
tatagatcaagcaggtttttaaatcctagtaggagcttacatttactttt 100
ccaaggggggagggggaataaatatctacacacacacacacacacacca 150
H4TF-1 GH
cactggagttcgagacgagggcctaagcaacatgccgaaaccccgctctta 200
DTF-1
ctaaatacaaaaaaatagctgagcttggtggcgacgcctatagtcctagc 250
tactggggaggctgaggtgggaggatcgcttgagcccaagaagtcgaggc 300
Sp1
tgcagtgagccgagatcgcgccgctgcactccagcctgagcgacagggcg 350
aggctctgtctcaaaacaaacaaacaaaaaaaaaaaaaggaaaggaaatata 400
 β -IFN
acacagtgaaatgaaaggattgagagaaatgaaaaatatacacgccacaa 450
HiNF-A
atgtgggagggcgataaccactcgtagaaagcgtgagaagttactacaag 500
cggtcctcccgggcaccgtactgttccgctcccagaagccccgggcgccg 550
AP-2
gaagtcgctcactcttaagaaggacggggccccacgctgcgcacccgcgg 600
E4F1
gtttgct ATG GCG ATG AGC AGC GGC GGC AGT GGT GGC 637
M A M S S G G S G G



REPLACEMENT SHEET

Figure 12A

cggcgtggtagcaggcc					ATG	GCG	ATG	GGC	AGT	GGC	GGA	GCG	41
					Met	Ala	Met	Gly	Ser	Gly	Gly	Ala	
GGC	TCC	GAG	CAG	GAA	GAT	ACG	GTG	CTG	TTC	CGG	CGT	GGC	80
Gly	Ser	Glu	Gln	Glu	Asp	Thr	Val	Leu	Phe	Arg	Arg	Gly	
ACC	GGC	CAG	AGT	GAT	GAT	TCT	GAC	ATT	TGG	GAT	GAT	ACA	119
Thr	Gly	Gln	Ser	Asp	Asp	Ser	Asp	Ile	Trp	Asp	Asp	Thr	
GCA	TTG	ATA	AAA	GCT	TAT	GAT	AAA	GCT	GTG	GCT	TCC	TTT	158
Ala	Leu	Ile	Lys	Ala	Tyr	Asp	Lys	Ala	Val	Ala	Ser	Phe	
AAG	CAT	GCT	CTA	AAG	AAC	GGT	GAC	ATT	TGT	GAA	ACT	CCA	197
Lys	His	Ala	Leu	Lys	Asn	Gly	Asp	Ile	Cys	Glu	Thr	Pro	
GAT	AAG	CCA	AAA	GGC	ACA	GCC	AGA	AGA	AAA	CCT	GCC	AAG	236
Asp	Lys	Pro	Lys	Gly	Thr	Ala	Arg	Arg	Lys	Pro	Ala	Lys	
AAG	AAT	AAA	AGC	CAA	AAG	AAG	AAT	GCC	ACA	ACT	CCC	TTG	275
Lys	Asn	Lys	Ser	Gln	Lys	Lys	Asn	Ala	Thr	Thr	Pro	Leu	
AAA	CAG	TGG	AAA	GTT	GGT	GAC	AAG	TGT	TCT	GCT	GTT	TGG	314
Lys	Gln	Trp	Lys	Val	Gly	Asp	Lys	Cys	Ser	Ala	Val	Trp	
TCA	GAA	GAC	GGC	TGC	ATT	TAC	CCA	GCT	ACT	ATT	ACG	TCC	353
Ser	Glu	Asp	Gly	Cys	Ile	Tyr	Pro	Ala	Thr	Ile	Thr	Ser	
ATT	GAC	TTT	AAG	AGA	GAA	ACC	TGT	GTC	GTG	GTT	TAT	ACT	392
Ile	Asp	Phe	Lys	Arg	Glu	Thr	Cys	Val	Val	Val	Tyr	Thr	
GGA	TAT	GGA	AAC	AGA	GAG	GAG	CAA	AAC	TTA	TCT	GAC	CTA	431
Gly	Tyr	Gly	Asn	Arg	Glu	Glu	Gln	Asn	Leu	Ser	Asp	Leu	
CTT	TCC	CCG	ACC	TGT	GAA	GTA	GCT	AAT	AGT	ACA	GAA	CAG	470
Leu	Ser	Pro	Thr	Cys	Glu	Val	Ala	Asn	Ser	Thr	Glu	Gln	
AAC	ACT	CAG	GAG	AAT	GAA	AGT	CAA	GTT	TCC	ACA	GAC	GAC	509
Asn	Thr	Gln	Glu	Asn	Glu	Ser	Gln	Val	Ser	Thr	Asp	Asp	
AGT	GAA	CAC	TCC	TCC	AGA	TCG	CTC	AGA	AGT	AAA	GCA	CAC	548
Ser	Glu	His	Ser	Ser	Arg	Ser	Leu	Arg	Ser	Lys	Ala	His	



REPLACEMENT SHEET

Figure 12B

AGC	AAG	TCC	AAA	GCT	GCT	CCG	TGG	ACC	TCA	TTT	CTT	CCT	587
Ser	Lys	Ser	Lys	Ala	Ala	Pro	Trp	Thr	Ser	Phe	Leu	Pro	
CCA	CCA	CCC	CCA	ATG	CCA	GGG	TCA	GGA	TTA	GGA	CCA	GGA	626
Pro	Pro	Pro	Pro	Met	Pro	Gly	Ser	Gly	Leu	Gly	Pro	Gly	
AAG	CCA	GGT	CTA	AAA	TTC	AAC	GGC	CCG	CCG	CCG	CCG	CCT	665
Lys	Pro	Gly	Leu	Lys	Phe	Asn	Gly	Pro	Pro	Pro	Pro	Pro	
CCA	CTA	CCC	CCT	CCC	CCC	TTC	CTG	CCG	TGC	TGG	ATG	CCC	704
Pro	Leu	Pro	Pro	Pro	Pro	Phe	Leu	Pro	Cys	Trp	Met	Pro	
CCG	TTC	CCT	TCA	GGA	CCA	CCA	ATA	ATC	CCG	CCA	CCC	CCT	743
Pro	Phe	Pro	Ser	Gly	Pro	Pro	Ile	Ile	Pro	Pro	Pro	Pro	
CCC	ATC	TCT	CCC	GAC	TGT	CTG	GAT	GAC	ACT	GAT	GCC	CTG	782
Pro	Ile	Ser	Pro	Asp	Cys	Leu	Asp	Asp	Thr	Asp	Ala	Leu	
GGC	AGT	ATG	CTA	ATC	TCT	TGG	TAC	ATG	AGT	GGC	TAC	CAC	821
Gly	Ser	Met	Leu	Ile	Ser	Trp	Tyr	Met	Ser	Gly	Tyr	His	
ACT	GGC	TAC	TAT	ATG	GGT	TTC	AGA	CAA	AAT	AAA	AAA	GAA	860
Thr	Gly	Tyr	Tyr	Met	Gly	Phe	Arg	Gln	Asn	Lys	Lys	Glu	
GGA	AAG	TGC	TCA	CAT	ACA	AAT	taag						885
Gly	Lys	Cys	Ser	His	Thr	Asn	*						

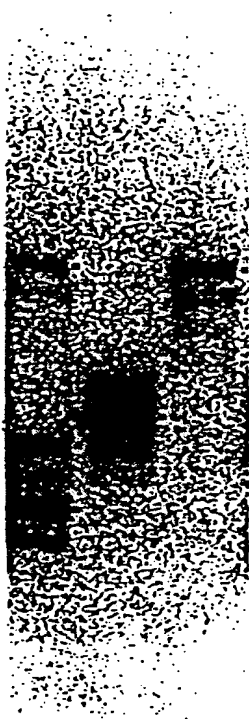


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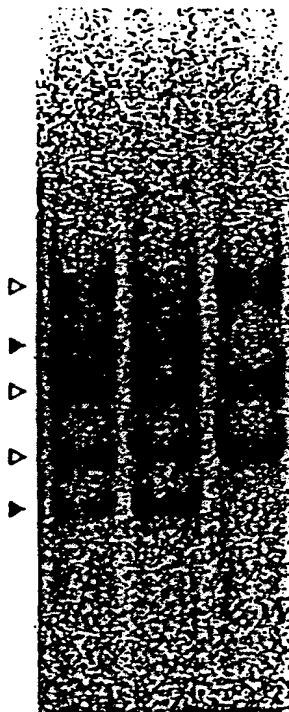
Figure 13

20	30	40	50	60	70
GSGGGVPEQEDSVLFRRGTGQSDDSDIWDDTALIKAYDKAVASFKHALKNGDICETS					
=====					
GSGGAGSEQEDTVLFRRGTGQSDDSDIWDDTALIKAYDKAVASFKHALKNGDICETP					
20	30	40	50	60	
80	90	100	110	120	130
GKPKTTPKRKPAKKNKSQKKNNTAASLQQWKVGDKCSAIWSEDGCIYPATIASIDFKR					
=====					
DKPKGTTARRKPAKKNKSQKKNATTPLKQWKVGDKCSAVWSEDGCIYPATITSIDFKR					
70		90	100	110	120
140	150	160	170	180	1
ETCVVVYTYGYNREEQNLSDLLSPICEVANNIEQNAQENENESQVSTDESENSRSPG					
=====					
ETCVVVYTYGYNREEQNLSDLLSPTCEVANSTEQNTQENE--SQVSTDDSEHSSRSL					
130	140		160	170	1
90	200	210	220	230	240
NKSDNIKPKSAPWNSFLPPPPMPGPRLGPGKPKGLKFNGPPPPPPPPPHLLSCWLP					
= =====					
RSKAHSKSKAAPWTSFLPPPPMPGSGLGPGKPKGLKFNGPPPPPLPPPPFLPCWMP					
80	190	200	210	220	230
250	260	270	280	290	300
PFPSGPPIIPPPPPICPDSLDDADALGSMLISWYMSGYHTGYIMGFRQNQKEGRCSH					
=====					
PFPSGPPIIPPPPPISPDCLDDTDALGSMLISWYMSGYHTGYIMGFRQNKKEGKCSH					
240	250	260	270	280	290

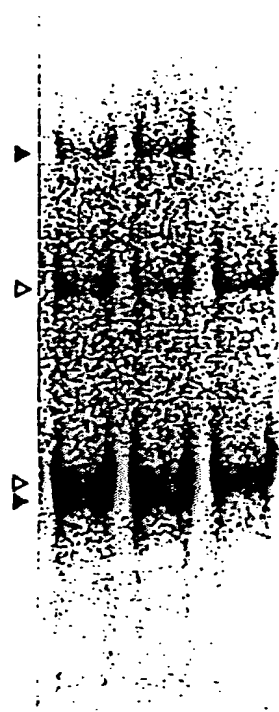
SL
-
TN



F M A



F M A



F M A

FIG. 14(A) FIG. 14(B) FIG. 14(C)



REPLACEMENT SHEET

SSCP ANALYSIS

▼ SMN
▽ C-BCD541



121B8 YAC
595CII YAC
HUMAN 1 CONTROL
HUMAN 2 CONTROL
HUMAN 3 CONTROL
HUMAN 4 SMA

FIG. 15

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